



(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (512) 418-3000
(B) TELEFAX: (713) 789-2679
(C) TELEX: 79-0924

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 186..1325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGCACCTTG CTGATCCCAA ACAGGCAGAG CTTCTTCCAG TCTTGGAAGG CACAAATTGA	60
GCATCAGGAA CGTGGACCCA TCAGGGCTGA ACAGCTACTC AGGATCTAAA GTGGTGACTT	120
GGAAAGCTGA CGGTGACTTG GGAAGGGAGG TCGCCAATCA GCGATCTGGA GCTGCAGCGC	180
TCACC ATG GAG TCC CCC ATT CAG ATC TTC CGA GGA GAT CCA GGC CCT	227
Met Glu Ser Pro Ile Gln Ile Phe Arg Gly Asp Pro Gly Pro	
1 5 10	
ACC TGC TCT CCC AGT GCT TGC CTT CTC CCC AAC AGC AGC TCT TGG TTC	275
Thr Cys Ser Pro Ser Ala Cys Leu Leu Pro Asn Ser Ser Ser Trp Phe	
15 20 25 30	
CCC AAC TGG GCA GAA TCC GAC AGT AAT GGC AGT GTG GGC TCA GAG GAT	323
Pro Asn Trp Ala Glu Ser Asp Ser Asn Gly Ser Val Gly Ser Glu Asp	
35 40 45	
CAG CAG CTG GAG TCC GCG CAC ATC TCT CCG GCC ATC CCT GTT ATC ATC	371
Gln Gln Leu Glu Ser Ala His Ile Ser Pro Ala Ile Pro Val Ile Ile	
50 55 60	
ACC GCT GTC TAC TCT GTG GTA TTT GTG GTG GGC TTA GTG GGC AAT TCT	419
Thr Ala Val Tyr Ser Val Val Phe Val Val Gly Leu Val Gly Asn Ser	
65 70 75	
CTG GTC ATG TTT GTC ATC ATC CGA TAC ACG AAG ATG AAG ACC GCA ACC	467
Leu Val Met Phe Val Ile Ile Arg Tyr Thr Lys Met Lys Thr Ala Thr	
80 85 90	
AAC ATC TAC ATA TTT AAC CTG GCT TTG GCA GAT GCT TTG GTT ACT ACC	515
Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Val Thr Thr	
95 100 105 110	

ACT	ATG	CCC	TTT	CAG	AGT	GCT	GTC	TAC	TTG	ATG	AAT	TCT	TGG	CCT	TTT	563
Thr	Met	Pro	Phe	Gln	Ser	Ala	Val	Tyr	Leu	Met	Asn	Ser	Trp	Pro	Phe	
				115					120					125		
GGA	GAT	GTG	CTA	TGC	AAG	ATT	GTC	ATT	TCC	ATT	GAC	TAC	TAC	AAC	ATG	611
Gly	Asp	Val	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	
			130					135					140			
TTT	ACC	AGC	ATA	TTC	ACC	TTG	ACC	ATG	ATG	AGT	GTG	GAC	CGC	TAC	ATT	659
Phe	Thr	Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	
		145					150					155				
GCT	GTG	TGC	CAC	CCT	GTG	AAA	GCT	TTG	GAC	TTC	CGA	ACA	CCT	TTG	AAA	707
Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Leu	Lys	
	160					165					170					
GCA	AAG	ATC	ATC	AAC	ATC	TGC	ATT	TGG	CTC	CTG	GCA	TCA	TCT	GTT	GGT	755
Ala	Lys	Ile	Ile	Asn	Ile	Cys	Ile	Trp	Leu	Leu	Ala	Ser	Ser	Val	Gly	
175					180					185					190	
ATA	TCA	GCG	ATA	GTC	CTT	GGA	GGC	ACC	AAA	GTC	AGG	GAA	GAT	GTG	GAT	803
Ile	Ser	Ala	Ile	Val	Leu	Gly	Gly	Thr	Lys	Val	Arg	Glu	Asp	Val	Asp	
				195					200					205		
GTC	ATT	GAA	TGC	TCC	TTG	CAG	TTT	CCT	GAT	GAT	GAA	TAT	TCC	TGG	TGG	851
Val	Ile	Glu	Cys	Ser	Leu	Gln	Phe	Pro	Asp	Asp	Glu	Tyr	Ser	Trp	Trp	
			210					215					220			
GAT	CTC	TTC	ATG	AAG	ATC	TGT	GTC	TTC	GTC	TTT	GCC	TTT	GTG	ATC	CCA	899
Asp	Leu	Phe	Met	Lys	Ile	Cys	Val	Phe	Val	Phe	Ala	Phe	Val	Ile	Pro	
		225					230					235				
GTC	CTC	ATC	ATC	ATT	GTC	TGC	TAC	ACC	CTG	ATG	ATC	CTG	CGC	CTG	AAG	947
Val	Leu	Ile	Ile	Ile	Val	Cys	Tyr	Thr	Leu	Met	Ile	Leu	Arg	Leu	Lys	
	240					245					250					
AGT	GTC	CGG	CTC	CTG	TCT	GGC	TCC	CGA	GAG	AAG	GAC	CGA	AAT	CTC	CGC	995
Ser	Val	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg	
255				260						265				270		
CGC	ATC	ACC	AAG	CTG	GTG	CTG	GTA	GTA	GTT	GCA	GTC	TTC	ATC	ATC	TGT	1043
Arg	Ile	Thr	Lys	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Ile	Cys	
				275					280					285		
TGG	ACC	CCC	ATT	CAC	ATC	TTT	ATC	CTG	GTG	GAG	GCT	CTG	GGA	AGC	ACC	1091
Trp	Thr	Pro	Ile	His	Ile	Phe	Ile	Leu	Val	Glu	Ala	Leu	Gly	Ser	Thr	
			290					295					300			
TCC	CAC	AGC	ACA	GCT	GCC	CTC	TCC	AGC	TAT	TAT	TTC	TGT	ATT	GCC	TTG	1139
Ser	His	Ser	Thr	Ala	Ala	Leu	Ser	Ser	Tyr	Tyr	Phe	Cys	Ile	Ala	Leu	
		305					310					315				
GGT	TAT	ACC	AAC	AGC	AGC	CTG	AAT	CCT	GTT	CTC	TAT	GCC	TTT	CTG	GAT	1187
Gly	Tyr	Thr	Asn	Ser	Ser	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	

320		325		330	
GAA AAC TTC AAG CGG TGT TTT AGG GAC TTC TGC TTC CCT ATT AAG ATG					1235
Glu Asn Phe Lys Arg Cys Phe Arg Asp Phe Cys Phe Pro Ile Lys Met					
335		340		345	350
CGA ATG GAG CGC CAG AGC ACC AAT AGA GTT AGA AAC ACA GTT CAG GAT					1283
Arg Met Glu Arg Gln Ser Thr Asn Arg Val Arg Asn Thr Val Gln Asp					
	355		360		365
CCT GCT TCC ATG AGA GAT GTG GGA GGG ATG AAT AAG CCA GTA					1325
Pro Ala Ser Met Arg Asp Val Gly Gly Met Asn Lys Pro Val					
	370		375		380
TGACTAGTCG TGGAAATGTC TTCTTATTGT TCTCCAGGTA GAGAAGAGTT CAATGATCTT					1385
GGTTTAACCC AGATTACAAC TGCAG					1410

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Ser	Pro	Ile	Gln	Ile	Phe	Arg	Gly	Asp	Pro	Gly	Pro	Thr	Cys
1				5					10					15	
Ser	Pro	Ser	Ala	Cys	Leu	Leu	Pro	Asn	Ser	Ser	Ser	Trp	Phe	Pro	Asn
			20					25					30		
Trp	Ala	Glu	Ser	Asp	Ser	Asn	Gly	Ser	Val	Gly	Ser	Glu	Asp	Gln	Gln
		35					40					45			
Leu	Glu	Ser	Ala	His	Ile	Ser	Pro	Ala	Ile	Pro	Val	Ile	Ile	Thr	Ala
	50					55					60				
Val	Tyr	Ser	Val	Val	Phe	Val	Val	Gly	Leu	Val	Gly	Asn	Ser	Leu	Val
65					70				75					80	
Met	Phe	Val	Ile	Ile	Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile
				85					90					95	
Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Val	Thr	Thr	Thr	Met
			100					105				110			
Pro	Phe	Gln	Ser	Ala	Val	Tyr	Leu	Met	Asn	Ser	Trp	Pro	Phe	Gly	Asp
		115					120					125			

Val	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr
130						135					140				
Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val
145					150					155					160
Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Leu	Lys	Ala	Lys
				165					170					175	
Ile	Ile	Asn	Ile	Cys	Ile	Trp	Leu	Leu	Ala	Ser	Ser	Val	Gly	Ile	Ser
			180					185					190		
Ala	Ile	Val	Leu	Gly	Gly	Thr	Lys	Val	Arg	Glu	Asp	Val	Asp	Val	Ile
		195					200					205			
Glu	Cys	Ser	Leu	Gln	Phe	Pro	Asp	Asp	Glu	Tyr	Ser	Trp	Trp	Asp	Leu
	210					215					220				
Phe	Met	Lys	Ile	Cys	Val	Phe	Val	Phe	Ala	Phe	Val	Ile	Pro	Val	Leu
225					230					235					240
Ile	Ile	Ile	Val	Cys	Tyr	Thr	Leu	Met	Ile	Leu	Arg	Leu	Lys	Ser	Val
				245					250					255	
Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile
			260					265					270		
Thr	Lys	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Ile	Cys	Trp	Thr
		275					280					285			
Pro	Ile	His	Ile	Phe	Ile	Leu	Val	Glu	Ala	Leu	Gly	Ser	Thr	Ser	His
	290					295					300				
Ser	Thr	Ala	Ala	Leu	Ser	Ser	Tyr	Tyr	Phe	Cys	Ile	Ala	Leu	Gly	Tyr
305					310					315					320
Thr	Asn	Ser	Ser	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn
				325					330					335	
Phe	Lys	Arg	Cys	Phe	Arg	Asp	Phe	Cys	Phe	Pro	Ile	Lys	Met	Arg	Met
			340					345					350		
Glu	Arg	Gln	Ser	Thr	Asn	Arg	Val	Arg	Asn	Thr	Val	Gln	Asp	Pro	Ala
		355					360					365			
Ser	Met	Arg	Asp	Val	Gly	Gly	Met	Asn	Lys	Pro	Val				
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2272 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 12..1127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACGCGGCGC	C	ATG	GAG	CTG	GTG	CCC	TCT	GCC	CGT	GCG	GAG	CTG	CAG	TCC	50	
	Met	Glu	Leu	Val	Pro	Ser	Ala	Arg	Ala	Glu	Leu	Gln	Ser			
	1				5						10					
TCG	CCC	CTC	GTC	AAC	CTC	TCG	GAC	GCC	TTT	CCC	AGC	GCC	TTC	CCC	AGC	98
Ser	Pro	Leu	Val	Asn	Leu	Ser	Asp	Ala	Phe	Pro	Ser	Ala	Phe	Pro	Ser	
	15				20						25					
GCG	GGC	GCC	AAT	GCG	TCG	GGG	TCG	CCG	GGA	GCC	CGT	AGT	GCC	TCG	TCC	146
Ala	Gly	Ala	Asn	Ala	Ser	Gly	Ser	Pro	Gly	Ala	Arg	Ser	Ala	Ser	Ser	
	30				35				40						45	
CTC	GCC	CTA	GCC	ATC	GCC	ATC	ACC	GCG	CTC	TAC	TCG	GCT	GTG	TGC	GCA	194
Leu	Ala	Leu	Ala	Ile	Ala	Ile	Thr	Ala	Leu	Tyr	Ser	Ala	Val	Cys	Ala	
				50					55					60		
GTG	GGG	CTT	CTG	GGC	AAC	GTG	CTC	GTC	ATG	TTT	GGC	ATC	GTC	CGG	TAC	242
Val	Gly	Leu	Leu	Gly	Asn	Val	Leu	Val	Met	Phe	Gly	Ile	Val	Arg	Tyr	
			65				70						75			
ACC	AAA	TTG	AAG	ACC	GCC	ACC	AAC	ATC	TAC	ATC	TTC	AAT	CTG	GCT	TTG	290
Thr	Lys	Leu	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	
		80					85					90				
GCT	GAT	GCG	CTG	GCC	ACC	AGC	ACG	CTG	CCC	TTC	CAG	AGC	GCC	AAG	TAC	338
Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Ala	Lys	Tyr	
	95					100					105					
TTG	ATG	GAA	ACG	TGG	CCG	TTT	GGC	GAG	CTG	CTG	TGC	AAG	GCT	GTG	CTC	386
Leu	Met	Glu	Thr	Trp	Pro	Phe	Gly	Glu	Leu	Leu	Cys	Lys	Ala	Val	Leu	
	110				115					120					125	
TCC	ATT	GAC	TAC	TAC	AAC	ATG	TTC	ACT	AGC	ATC	TTC	ACC	CTC	ACC	ATG	434
Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Thr	Met	
				130					135					140		
ATG	AGC	GTG	GAC	CGC	TAC	ATT	GCT	GTC	TGC	CAT	CCT	GTC	AAA	GCC	CTG	482
Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu	
			145					150					155			
GAC	TTC	CGG	ACA	CCA	GCC	AAG	GCC	AAG	CTG	ATC	AAT	ATA	TGC	ATC	TGG	530
Asp	Phe	Arg	Thr	Pro	Ala	Lys	Ala	Lys	Leu	Ile	Asn	Ile	Cys	Ile	Trp	
		160					165					170				

GTC Val	TTG Leu	GCT Ala	TCA Ser	GGT Gly	GTC Val	GGG Gly	GTC Val	CCC Pro	ATC Ile	ATG Met	GTC Val	ATG Met	GCA Ala	GTG Val	ACC Thr	578
175180185																
CAA Gln	CCC Pro	CGG Arg	GAT Asp	GGT Gly	GCA Ala	GTG Val	GTA Val	TGC Cys	ATG Met	CTC Leu	CAG Gln	TTC Phe	CCC Pro	AGT Ser	CCC Pro	626
190195200205																
AGC Ser	TGG Trp	TAC Tyr	TGG Trp	GAC Asp	ACT Thr	GTG Val	ACC Thr	AAG Lys	ATC Ile	TGC Cys	GTG Val	TTC Phe	CTC Leu	TTT Phe	GCC Ala	674
210215220																
TTC Phe	GTG Val	GTG Val	CCG Pro	ATC Ile	CTC Leu	ATC Ile	ATC Ile	ACG Thr	GTG Val	TGC Cys	TAT Tyr	GGC Gly	CTC Leu	ATG Met	CTA Leu	722
225230235																
CTG Leu	CGC Arg	CTG Leu	CGC Arg	AGC Ser	GTG Val	CGT Arg	CTG Leu	CTG Leu	TCC Ser	GGT Gly	TCC Ser	AAG Lys	GAG Glu	AAG Lys	GAC Asp	770
240245250																
CGC Arg	AGC Ser	CTG Leu	CGG Arg	CGC Arg	ATC Ile	ACG Thr	CGC Arg	ATG Met	GTG Val	CTG Leu	GTG Val	GTG Val	GTG Val	GGC Gly	GCC Ala	818
255260265																
TTC Phe	GTG Val	GTG Val	TGC Cys	TGG Trp	GCG Ala	CCC Pro	ATC Ile	CAC His	ATC Ile	TTC Phe	GTC Val	ATC Ile	GTC Val	TGG Trp	ACG Thr	866
270275280285																
CTG Leu	GTG Val	GAC Asp	ATC Ile	AAT Asn	CGG Arg	CGC Arg	GAC Asp	CCA Pro	CTT Leu	GTG Val	GTG Val	GCC Ala	GCA Ala	CTG Leu	CAC His	914
290295300																
CTG Leu	TGC Cys	ATT Ile	GCG Ala	CTG Leu	GGC Gly	TAC Tyr	GCC Ala	AAC Asn	AGC Ser	AGC Ser	CTC Leu	AAC Asn	CCG Pro	GTT Val	CTC Leu	962
305310315																
TAC Tyr	GCC Ala	TTC Phe	CTG Leu	GAC Asp	GAG Glu	AAC Asn	TTC Phe	AAG Lys	CGC Arg	TGC Cys	TTC Phe	CGC Arg	CAG Gln	CTC Leu	TGT Cys	1010
320325330																
CGC Arg	ACG Thr	CCC Pro	TGC Cys	GGC Gly	CGC Arg	CAA Gln	GAA Glu	CCC Pro	GGC Gly	AGT Ser	CTC Leu	CGT Arg	CGT Arg	CCC Pro	CGC Arg	1058
335340345																
CAG Gln	GCC Ala	ACC Thr	ACG Thr	CGT Arg	GAG Glu	CGT Arg	GTC Val	ACT Thr	GCC Ala	TGC Cys	ACC Thr	CCC Pro	TCC Ser	GAC Asp	GGC Gly	1106
350355360365																
CCG Pro	GGC Gly	GGT Gly	GGC Gly	GCT Ala	GCC Ala	GCC Ala	TGACCTACCC GACCTTCCCC TTAAACGCCC									1157
370																
CTCCCAAGTG AAGTGATCCA GAGGCCACAC CGAGCTCCCT GGGAGGCTGT GGCCACCACC																1217

AGGACAGCTA GAATTGGGCC TGCACAGAGG GGAGGCCTCC TGTGGGGACG GGGCCTGAGG	1277
GATCAAAGGC TCCAGGTTGG AACGGTGGGG GTGAGGAAGC AGAGCTGGTG ATTCCTAAAC	1337
TGTATCCATT AGTAAGGCCT CTCCAATGGG ACAGAGCCTC CGCCTTGAGA TAACATCGGG	1397
TTCTGGCCAA AAAGAACACC AGCTCCAGTC CAAGACCCAA GGATTCCAGC TCCAGGAACC	1457
AGGAGGGGTC GATGATTTGG TTTGGCTGAG AGTCCCAGCA TTTGTGTTAT GGGGAGGATC	1517
TCTCATCTTA GAGAAGATAA GGGGACAGGG CATTCAGGCA AGGCAGCTTG GGGTTTGGTC	1577
AGGAGATAAG CGCCCCCTTC CTTTGGGGGG AGGATAAGTG GGGGATGGTC AACGTTGGAG	1637
AAGAGTCAAA GTTCTCACCA CCTTTCTAAC TACTCAGCTA AACTCGTTGA GGCTAGGGCA	1697
ACGTGACTTC TCTGTAGAGA GGATACAAGC CGGGCCTGAT GGGGCAGGCT GTGTAATCCC	1757
AGTCATAGTG GAGGCTGAGG CTGGAAAATT AAGGACCAAC AGCCTGGGCA ATTTAGTGTC	1817
TCAAAATAAA ATGTAAAGAG GGCTGGGAAT GTAGCTCAGT GGTAGGGTGT TTGTGTGAGG	1877
CTCTGGGATC AATAAGACAA AACAAACCAAC CAACCAAAAA CCTTCCAAAC AACAAAACCA	1937
ACCCTCAAAC CAAAAAATA TGTGGGTGTC TCTGAGTCTG GTTTGAAGAG AACCCGCAGC	1997
CCTGTATCCC TGTGGGGCTG TGGACAGTGG GCAGAAGCAG AGGCTCCCTG GATCCTGAAC	2057
AAGGGCCCCA AAAGCAAGTT CTAAAGGGAC CCCTGAAACC GAGTAAGCCT TTGTGTCAAG	2117
AAGTGGGAGT AGAACCAGAA AGGTGGCTGA GTGATTAAGG GCACGTGACT CTCTTGACAG	2177
GGACATAGGT TCGATTCCCA GCACCCACAT AGTGGCTCAC AGCCATCTGT AACCCAGTC	2237
GCAGTCAATC TAATGCTTTC CAACAACTGT GGGCA	2272

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Leu	Val	Pro	Ser	Ala	Arg	Ala	Glu	Leu	Gln	Ser	Ser	Pro	Leu
1				5					10					15	
Val	Asn	Leu	Ser	Asp	Ala	Phe	Pro	Ser	Ala	Phe	Pro	Ser	Ala	Gly	Ala
			20					25					30		

Asn Ala Ser Gly Ser Pro Gly Ala Arg Ser Ala Ser Ser Leu Ala Leu
 35 40 45
 Ala Ile Ala Ile Thr Ala Leu Tyr Ser Ala Val Cys Ala Val Gly Leu
 50 55 60
 Leu Gly Asn Val Leu Val Met Phe Gly Ile Val Arg Tyr Thr Lys Leu
 65 70 75 80
 Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala
 85 90 95
 Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Ala Lys Tyr Leu Met Glu
 100 105 110
 Thr Trp Pro Phe Gly Glu Leu Leu Cys Lys Ala Val Leu Ser Ile Asp
 115 120 125
 Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Thr Met Met Ser Val
 130 135 140
 Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg
 145 150 155 160
 Thr Pro Ala Lys Ala Lys Leu Ile Asn Ile Cys Ile Trp Val Leu Ala
 165 170 175
 Ser Gly Val Gly Val Pro Ile Met Val Met Ala Val Thr Gln Pro Arg
 180 185 190
 Asp Gly Ala Val Val Cys Met Leu Gln Phe Pro Ser Pro Ser Trp Tyr
 195 200 205
 Trp Asp Thr Val Thr Lys Ile Cys Val Phe Leu Phe Ala Phe Val Val
 210 215 220
 Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Leu Leu Arg Leu
 225 230 235 240
 Arg Ser Val Arg Leu Leu Ser Gly Ser Lys Glu Lys Asp Arg Ser Leu
 245 250 255
 Arg Arg Ile Thr Arg Met Val Leu Val Val Val Gly Ala Phe Val Val
 260 265 270
 Cys Trp Ala Pro Ile His Ile Phe Val Ile Val Trp Thr Leu Val Asp
 275 280 285
 Ile Asn Arg Arg Asp Pro Leu Val Val Ala Ala Leu His Leu Cys Ile
 290 295 300
 Ala Leu Gly Tyr Ala Asn Ser Ser Leu Asn Pro Val Leu Tyr Ala Phe
 305 310 315 320

Met 70	Tyr	Val	Ile	Leu	Arg 75	His	Thr	Lys	Met	Lys 80	Thr	Ala	Thr	Asn	Ile 85	
TAC	ATA	TTT	AAT	CTG	GCA	CTG	GCT	GAT	ACC	CTG	GTC	TTG	CTG	ACA	CTG	463
Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Thr	Leu	Val	Leu	Leu	Thr	Leu	
				90					95					100		
CCC	TTC	CAG	GGC	ACA	GAC	ATC	CTT	CTG	GGC	TTC	TGG	CCA	TTT	GGG	AAT	511
Pro	Phe	Gln	Gly	Thr	Asp	Ile	Leu	Leu	Gly	Phe	Trp	Pro	Phe	Gly	Asn	
			105					110					115			
GCA	CTG	TGC	AAG	ACG	GTC	ATT	GCT	ATC	GAC	TAC	TAC	AAC	ATG	TTT	ACC	559
Ala	Leu	Cys	Lys	Thr	Val	Ile	Ala	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	
		120					125					130				
AGC	ACT	TTC	ACT	TTG	ACT	GCC	ATG	AGT	GTA	GAC	CGT	TAT	GTA	GCT	ATC	607
Ser	Thr	Phe	Thr	Leu	Thr	Ala	Met	Ser	Val	Asp	Arg	Tyr	Val	Ala	Ile	
	135					140					145					
TGC	CAC	CCT	ATC	CGT	GCC	CTT	GAT	GTT	CGG	ACA	TCC	AGT	AAA	GCC	CAG	655
Cys	His	Pro	Ile	Arg	Ala	Leu	Asp	Val	Arg	Thr	Ser	Ser	Lys	Ala	Gln	
150					155					160					165	
GCC	GTT	AAT	GTG	GCC	ATA	TGG	GCC	CTG	GCT	TCG	GTG	GTT	GGT	GTT	CCT	703
Ala	Val	Asn	Val	Ala	Ile	Trp	Ala	Leu	Ala	Ser	Val	Val	Gly	Val	Pro	
				170					175					180		
GTT	GCC	ATC	ATG	GGC	TCA	GCA	CAA	GTG	GAG	GAT	GAA	GAG	ATC	GAG	TGC	751
Val	Ala	Ile	Met	Gly	Ser	Ala	Gln	Val	Glu	Asp	Glu	Glu	Ile	Glu	Cys	
			185					190					195			
CTG	GTG	GAG	ATC	CCC	GCC	CCT	CAG	GAC	TAT	TGG	GGC	CCT	GTA	TTT	GCC	799
Leu	Val	Glu	Ile	Pro	Ala	Pro	Gln	Asp	Tyr	Trp	Gly	Pro	Val	Phe	Ala	
		200					205					210				
ATC	TGC	ATC	TTC	CTT	TTT	TCC	TTC	ATC	ATC	CCG	GTT	CTG	ATC	ATC	TCT	847
Ile	Cys	Ile	Phe	Leu	Phe	Ser	Phe	Ile	Ile	Pro	Val	Leu	Ile	Ile	Ser	
	215					220					225					
GTC	TGC	TAC	AGC	CTC	ATG	ATT	CGA	CGA	CTT	CGT	GGT	GTC	CGG	CTG	CTT	895
Val	Cys	Tyr	Ser	Leu	Met	Ile	Arg	Arg	Leu	Arg	Gly	Val	Arg	Leu	Leu	
230					235					240				245		
TCA	GGC	TCC	CGA	GAG	AAG	GAC	CGG	AAC	CTG	CGA	CGC	ATC	ACA	CGG	CTG	943
Ser	Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Leu	
				250					255					260		
GTA	CTG	GTA	GTT	GTG	GCT	GTG	TTT	GTG	GGC	TGC	TGG	ACA	CCT	GTG	CAG	991
Val	Leu	Val	Val	Val	Ala	Val	Phe	Val	Gly	Cys	Trp	Thr	Pro	Val	Gln	
			265					270					275			
GTC	TTT	GTC	CTG	GTT	CAA	GGA	CTG	GGT	GTT	CAG	CCA	GGT	AGT	GAG	ACT	1039
Val	Phe	Val	Leu	Val	Gln	Gly	Leu	Gly	Val	Gln	Pro	Gly	Ser	Glu	Thr	
		280					285					290				

GCA	GTA	GCC	ATT	CTG	CGC	TTC	TGC	ACA	GCC	CTG	GGC	TAT	GTC	AAC	AGT	1087
Ala	Val	Ala	Ile	Leu	Arg	Phe	Cys	Thr	Ala	Leu	Gly	Tyr	Val	Asn	Ser	
295						300					305					
TGT	CTC	AAT	CCC	ATT	CTC	TAT	GCT	TTC	TTG	GAT	GAG	AAC	TTC	AAG	GCC	1135
Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Ala	
310					315					320					325	
TGC	TTT	AGA	AAG	TTC	TGC	TGT	GCT	TCT	GCC	CTG	CAC	CGG	GAG	ATG	CAG	1183
Cys	Phe	Arg	Lys	Phe	Cys	Cys	Ala	Ser	Ala	Leu	His	Arg	Glu	Met	Gln	
				330					335					340		
GTT	TCT	GAT	CGT	GTG	CGC	AGC	ATT	GCC	AAG	GAT	GTA	GGC	CTT	GGT	TGC	1231
Val	Ser	Asp	Arg	Val	Arg	Ser	Ile	Ala	Lys	Asp	Val	Gly	Leu	Gly	Cys	
			345					350					355			
AAG	ACC	TCT	GAG	ACA	GTA	CCA	CGG	CCG	GCA	TGACTAGGCG	TGGACCTGCC					1281
Lys	Thr	Ser	Glu	Thr	Val	Pro	Arg	Pro	Ala							
		360					365									
CATGGTGCCT	GTCAGTCCAC	AGAGCCCATC	TACACCCAAC	ACGGAGCTC												1330

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Ser	Leu	Phe	Pro	Ala	Pro	Phe	Trp	Glu	Val	Leu	Tyr	Gly	Ser	
1				5					10					15		
His	Phe	Gln	Gly	Asn	Leu	Ser	Leu	Leu	Asn	Glu	Thr	Val	Pro	His	His	
		20					25						30			
Leu	Leu	Leu	Asn	Ala	Ser	His	Ser	Ala	Phe	Leu	Pro	Leu	Gly	Leu	Lys	
		35					40					45				
Val	Thr	Ile	Val	Gly	Leu	Tyr	Leu	Ala	Val	Cys	Ile	Gly	Gly	Leu	Leu	
	50				55						60					
Gly	Asn	Cys	Leu	Val	Met	Tyr	Val	Ile	Leu	Arg	His	Thr	Lys	Met	Lys	
65					70					75					80	
Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Thr	Leu	
			85						90					95		
Val	Leu	Leu	Thr	Leu	Pro	Phe	Gln	Gly	Thr	Asp	Ile	Leu	Leu	Gly	Phe	
			100					105						110		

Trp Pro Phe Gly Asn Ala Leu Cys Lys Thr Val Ile Ala Ile Asp Tyr
 115 120 125
 Tyr Asn Met Phe Thr Ser Thr Phe Thr Leu Thr Ala Met Ser Val Asp
 130 135 140
 Arg Tyr Val Ala Ile Cys His Pro Ile Arg Ala Leu Asp Val Arg Thr
 145 150 155 160
 Ser Ser Lys Ala Gln Ala Val Asn Val Ala Ile Trp Ala Leu Ala Ser
 165 170 175
 Val Val Gly Val Pro Val Ala Ile Met Gly Ser Ala Gln Val Glu Asp
 180 185 190
 Glu Glu Ile Glu Cys Leu Val Glu Ile Pro Ala Pro Gln Asp Tyr Trp
 195 200 205
 Gly Pro Val Phe Ala Ile Cys Ile Phe Leu Phe Ser Phe Ile Ile Pro
 210 215 220
 Val Leu Ile Ile Ser Val Cys Tyr Ser Leu Met Ile Arg Arg Leu Arg
 225 230 235 240
 Gly Val Arg Leu Leu Ser Gly Ser Arg Glu Lys Asp Arg Asn Leu Arg
 245 250 255
 Arg Ile Thr Arg Leu Val Leu Val Val Val Ala Val Phe Val Gly Cys
 260 265 270
 Trp Thr Pro Val Gln Val Phe Val Leu Val Gln Gly Leu Gly Val Gln
 275 280 285
 Pro Gly Ser Glu Thr Ala Val Ala Ile Leu Arg Phe Cys Thr Ala Leu
 290 295 300
 Gly Tyr Val Asn Ser Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu Asp
 305 310 315 320
 Glu Asn Phe Lys Ala Cys Phe Arg Lys Phe Cys Cys Ala Ser Ala Leu
 325 330 335
 His Arg Glu Met Gln Val Ser Asp Arg Val Arg Ser Ile Ala Lys Asp
 340 345 350
 Val Gly Leu Gly Cys Lys Thr Ser Glu Thr Val Pro Arg Pro Ala
 355 360 365

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGGGCAATT CACTAGTCAT GTTT

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTGGGCAACG TACTAGTCAT GTTT

24

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Y
- (B) LOCATION: 6, 12, 15, and 18
- (C) IDENTIFICATION METHOD: Y = T or C

(ix) FEATURE:

- (A) NAME/KEY: R
- (B) LOCATION: 7
- (C) IDENTIFICATION METHOD: R = G or A

(ix) FEATURE:

- (A) NAME/KEY: N
- (B) LOCATION: 21
- (C) IDENTIFICATION METHOD: N = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCAAARTCT AYATYATYCT NAACCTGGC

29

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: N
 - (B) LOCATION: 3
 - (C) IDENTIFICATION METHOD: N = Inosine
- (ix) FEATURE:
 - (A) NAME/KEY: R
 - (B) LOCATION: 9 and 18
 - (C) IDENTIFICATION METHOD: R = G or A
- (ix) FEATURE:
 - (A) NAME/KEY: W
 - (B) LOCATION: 13
 - (C) IDENTIFICATION METHOD: W = A or T
- (ix) FEATURE:
 - (A) NAME/KEY: K
 - (B) LOCATION: 15
 - (C) IDENTIFICATION METHOD: K = G or T
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACNGTCAGRC AGWAKATRCT GGTGAA

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1000 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: N
 - (B) LOCATION: 607-608, 642-643, 896, 906
 - (C) IDENTIFICATION METHOD: N = A, C, G or T
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 102..986

(ix) FEATURE:

- (A) NAME/KEY: Xaa
(B) LOCATION: 169, 181, 265, 269
(C) IDENTIFICATION METHOD: Xaa = unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGAAGCAAA ATCAGTAATC CAAAGGCTAT CACAAACACA TTCACCTTAT GGGGTTTGAC	60
TTGAAAATGG AGGGAAATGC TATTGTTTCT TTTCTTTTAG A TAC ACA AAG ATG AAG	116
Tyr Thr Lys Met Lys	5
ACA GCA ACC AAC ATT TAC ATA TTT AAC CTG GCT TTG GCA GAT GCT TTA	164
Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu	10 15 20
GTT ACT ACA ACC ATG CCC TTT CAG AGT ACG GTC TAC TTG ATG AAT TCC	212
Val Thr Thr Thr Met Pro Phe Gln Ser Thr Val Tyr Leu Met Asn Ser	25 30 35
TGG CCT TTT GGG GAT GTG CTG TGC AAG ATA GTA ATT TCC ATT GAT TAC	260
Trp Pro Phe Gly Asp Val Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr	40 45 50
TAC AAC ATG TTC ACC AGC ATC TTC ACC TTG ACC ATG ATG AGC GTG GAC	308
Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Thr Met Met Ser Val Asp	55 60 65
CGC TAC ATT GCC GTG TGC CAC CCC GTG AAG GCT TTG GAC TTC CGC ACA	356
Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg Thr	70 75 80 85
CCC TTG AAG GCA AAG ATC ATC AAT ATC TGC ATC TGG CTG CTG TCG TCA	404
Pro Leu Lys Ala Lys Ile Ile Asn Ile Cys Ile Trp Leu Leu Ser Ser	90 95 100
TCT GTT GGC ATC TCT GCA ATA GTC CTT GGA GGC ACC AAA GTC AGG GAA	452
Ser Val Gly Ile Ser Ala Ile Val Leu Gly Gly Thr Lys Val Arg Glu	105 110 115
GGT GTC GAT GTC ATT GAG TGC TGC TTG CAG TTC CCA GAT GAT GAC TAC	500
Asp Val Asp Val Ile Glu Cys Cys Leu Gln Phe Pro Asp Asp Asp Tyr	120 125 130
TCC TGG TGG GAC CTC TTC ATG AAG ATC TGC GTC TTC ATC TTT GCC TTC	548
Ser Trp Trp Asp Leu Phe Met Lys Ile Cys Val Phe Ile Phe Ala Phe	135 140 145
GTG ATC CCT GTC CTC ATC ATC ATC GTC TGC TAC ACC CTG ATG ATC CTG	596
Val Ile Pro Val Leu Ile Ile Ile Val Cys Tyr Thr Leu Met Ile Leu	150 155 160 165
CGT CTC AAG ANN GTC CGG CTC CTT TCT GGC TCC CGA GAG AAA GAT NNC	644

Arg	Leu	Lys	Xaa	Val	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	Xaa		
				170					175					180			
AAC	CTG	CGT	AGG	ATC	ACC	AGA	CTG	GTC	CTG	GTG	GTG	GTG	GCA	GTC	TTC		692
Asn	Leu	Arg	Arg	Ile	Thr	Arg	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe		
			185					190					195				
GTC	GTC	TGC	TGG	ACT	CCC	ATT	CAC	ATA	TTC	ATC	CTG	GTG	GAG	GCT	CTG		740
Val	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Phe	Ile	Leu	Val	Glu	Ala	Leu		
		200					205					210					
GGG	AGC	ACC	TCC	CAC	AGC	ACA	GCT	GCT	CTC	TCC	AGC	TAT	TAC	TTC	TGC		788
Gly	Ser	Thr	Ser	His	Ser	Thr	Ala	Ala	Leu	Ser	Ser	Tyr	Tyr	Phe	Cys		
	215					220					225						
ATC	GCC	TTA	GGC	TAT	ACC	AAC	AGT	AGC	CTG	AAT	CCC	ATT	CTC	TAC	GCC		836
Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Ser	Leu	Asn	Pro	Ile	Leu	Tyr	Ala		
230					235					240					245		
TTT	CTT	GAT	GAA	AAC	TTC	AAG	CGG	TGT	TTC	CGG	GAC	TTC	TGC	TTT	CCA		884
Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Asp	Phe	Cys	Phe	Pro		
				250					255					260			
CTG	AAG	ATG	AGN	ATG	GAG	CGC	NAG	AGC	ACT	AGC	AGA	GTC	CGA	AAT	ACA		932
Leu	Lys	Met	Xaa	Met	Glu	Arg	Xaa	Ser	Thr	Ser	Arg	Val	Arg	Asn	Thr		
			265					270					275				
GTT	CAG	GAT	CCT	GCT	TAC	CTG	AGG	GAG	ATC	GAT	GGG	ATG	ATG	AAT	AAA		980
Val	Gln	Asp	Pro	Ala	Tyr	Leu	Arg	Glu	Ile	Asp	Gly	Met	Met	Asn	Lys		
		280					285					290					
CCA	GTA	TGACTAGTCG	TGGA														1000
Pro	Val																
	295																

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Xaa

(B) LOCATION: 169, 181, 265, 269

(C) IDENTIFICATION METHOD: Xaa = unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala		
				5					10						15		

Leu Ala Asp Ala Leu Val Thr Thr Thr Met Pro Phe Gln Ser Thr Val
 20 25 30
 Tyr Leu Met Asn Ser Trp Pro Phe Gly Asp Val Leu Cys Lys Ile Val
 35 40 45
 Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Thr
 50 55 60
 Met Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala
 65 70 75 80
 Leu Asp Phe Arg Thr Pro Leu Lys Ala Lys Ile Ile Asn Ile Cys Ile
 85 90 95
 Trp Leu Leu Ser Ser Ser Val Gly Ile Ser Ala Ile Val Leu Gly Gly
 100 105 110
 Thr Lys Val Arg Glu Asp Val Asp Val Ile Glu Cys Cys Leu Gln Phe
 115 120 125
 Pro Asp Asp Asp Tyr Ser Trp Trp Asp Leu Phe Met Lys Ile Cys Val
 130 135 140
 Phe Ile Phe Ala Phe Val Ile Pro Val Leu Ile Ile Ile Val Cys Tyr
 145 150 155 160
 Thr Leu Met Ile Leu Arg Leu Lys Xaa Val Arg Leu Leu Ser Gly Ser
 165 170 175
 Arg Glu Lys Asp Xaa Asn Leu Arg Arg Ile Thr Arg Leu Val Leu Val
 180 185 190
 Val Val Ala Val Phe Val Val Cys Trp Thr Pro Ile His Ile Phe Ile
 195 200 205
 Leu Val Glu Ala Leu Gly Ser Thr Ser His Ser Thr Ala Ala Leu Ser
 210 215 220
 Ser Tyr Tyr Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Ser Leu Asn
 225 230 235 240
 Pro Ile Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg
 245 250 255
 Asp Phe Cys Phe Pro Leu Lys Met Xaa Met Glu Arg Xaa Ser Thr Ser
 260 265 270
 Arg Val Arg Asn Thr Val Gln Asp Pro Ala Tyr Leu Arg Glu Ile Asp
 275 280 285
 Gly Met Met Asn Lys Pro Val
 290 295

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Ile Ile Ala Lys Met Arg Met Val Ala Leu Lys Ala Gly Trp Gln
 5 10 15
Gln Arg Lys Arg Ser Glu Arg Lys Ile Thr Leu Met
 20 25

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Met Ile Leu Arg Leu Lys Ser Val Arg Leu Leu Ser Gly Ser Arg
 5 10 15
Glu Lys Asp Arg Asn Leu Arg Arg Ile Thr Lys Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Met Leu Leu Arg Leu Arg Ser Val Arg Leu Leu Ser Gly Ser Lys
 5 10 15
Glu Lys Asp Arg Ser Leu Arg Arg Ile Thr Arg Met
 20 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asp Arg Tyr Val Ala Val Val His Pro Ile Lys Ala Ala Arg Tyr Arg
 5 10 15
Arg Pro

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg
 5 10 15
Thr Pro

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TATCTAGGTC GACGG

15

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CATCTTAGCA ATGAT

15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTCGAGAATT CCCCC

15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGCGCAGT AGCAT

15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TAGGTCGACG GTATC

15

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGCGCAGG ATCAT

15

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCATGGTGG CCCTC

15

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTGATCTTG CGCTC

15

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGCAGCGTGC GTCTG

15

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGTGATCCGC CGCAG

15

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGAGTGTCC GGCTC

15

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGTGATCCGG CGGAG

15

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGCGCAAGA TCACC

15

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCGAGAATTC CCCGG

15

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGCGGCGCG ATCAC

15

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TAGGTCGACG GTGTGG

16

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCCGGCGGA TCACC

15

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGTCGAGAA CTAGT

15

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Tyr Pro Gly Ser Asn Thr Tyr Glu Asp
5 10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Tyr Thr Gly Pro Ser Ala Phe Thr Glu
5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Thr Val Gln Asp Pro Ala Ser Met Arg Asp Val Gly
5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Pro Ile Gln Ile Phe Arg Gly Asp Pro Gly Pro Thr Cys Ser
5 10 15

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ser Asp Ala Phe Pro Ser Ala Phe Pro Ser Ala Gly Ala
5 10

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala Thr Thr Arg Glu Arg Val Thr Ala Cys Thr Pro Ser
 5 10

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTGGGCAACG TACTAGTCAT GTTTGGC

27

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTGGGCAATT CACTAGTCAT GTTTGTC

27

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCTCTCCATT AACTACTACA A

21

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGCGCCCATC AACATCTTCG T

21

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acids
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ala Thr Thr Arg Glu Arg Val Thr Ala Cys Thr Pro Ser
1 5 10